

SEQUENCE LISTING

<110> Klee, Harry J.
Lashbrook, Coralie
Shrode, Lori

<120> Materials and Methods for Tissue-Specific Targeting of Ethylene
Insensitivity in Transgenic Plants

<130> UF-325XC1

<150> US 60/390,385

<151> 2002-06-21

<160> 9

<170> PatentIn version 3.2

<210> 1

<211> 738

<212> PRT

<213> pLBS107 construct

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Phe	Ser	Ile	Pro	Leu	Glu	Leu	Ile	Tyr	Phe	Val	Lys	Lys	Ser	Ala	Val	35	40	45	
Phe	Pro	Tyr	Arg	Trp	Val	Leu	Val	Gln	Phe	Gly	Ala	Phe	Ile	Val	Leu	50	55	60	
Tyr	Gly	Ala	Thr	His	Leu	Ile	Asn	Leu	Trp	Thr	Phe	Thr	Thr	His	Ser	65	70	75	80
Arg	Thr	Val	Ala	Leu	Val	Met	Thr	Thr	Ala	Lys	Val	Leu	Thr	Ala	Val	85	90	95	
Val	Ser	Cys	Ala	Thr	Ala	Leu	Met	Leu	Val	His	Ile	Ile	Pro	Asp	Leu	100	105	110	
Leu	Ser	Val	Lys	Thr	Arg	Glu	Leu	Phe	Leu	Lys	Asn	Lys	Ala	Ala	Glu	115	120	125	
Leu	Asp	Arg	Glu	Met	Gly	Leu	Ile	Arg	Thr	Gln	Glu	Glu	Thr	Gly	Arg	130	135	140	
His	Val	Arg	Met	Leu	Thr	His	Glu	Ile	Arg	Ser	Thr	Leu	Asp	Arg	His	145	150	155	160

Thr Ile Leu Lys Thr Thr Leu Val Glu Leu Gly Arg Thr Leu Ala Leu
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 Glu Glu Cys Ala Leu Trp Met Pro Thr Arg Thr Gly Leu Glu Leu Gln
 180 185 190
 Leu Ser Tyr Thr Leu Arg His Gln His Pro Val Glu Tyr Thr Val Pro
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 Ile Gln Leu Pro Val Ile Asn Gln Val Phe Gly Thr Ser Arg Ala Val
 210 215 220
 Lys Ile Ser Pro Asn Ser Pro Val Ala Arg Leu Arg Pro Val Ser Gly
 225 230 235 240
 Lys Tyr Met Leu Gly Glu Val Val Ala Val Arg Val Pro Leu Leu His
 245 250 255
 Leu Ser Asn Phe Gln Ile Asn Asp Trp Pro Glu Leu Ser Thr Lys Arg
 260 265 270
 Tyr Ala Leu Met Val Leu Met Leu Pro Ser Asp Ser Ala Arg Gln Trp
 275 280 285
 His Val His Glu Leu Glu Leu Val Glu Val Val Ala Asp Gln Val Ala
 290 295 300
 Val Ala Leu Ser His Ala Ala Ile Leu Glu Glu Ser Met Arg Ala Arg
 305 310 315 320
 Asp Leu Leu Met Glu Gln Asn Val Ala Leu Asp Leu Ala Arg Arg Glu
 325 330 335
 Ala Glu Thr Ala Ile Arg Ala Arg Asn Asp Phe Leu Ala Val Met Asn
 340 345 350
 His Glu Met Arg Thr Pro Met His Ala Ile Ile Ala Leu Ser Ser Leu
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 370 375 380
 Ile Leu Lys Ser Ser Asn Leu Leu Ala Thr Leu Met Asn Asp Val Leu
 385 390 395 400
 Asp Leu Ser Arg Leu Glu Asp Gly Ser Leu Gln Leu Glu Leu Gly Thr
 405 410 415
 Phe Asn Leu His Thr Leu Phe Arg Glu Val Leu Asn Leu Ile Lys Pro
 420 425 430
 Ile Ala Val Val Lys Lys Leu Pro Ile Thr Leu Asn Leu Ala Pro Asp
 435 440 445
 Leu Pro Glu Phe Val Val Gly Asp Glu Lys Arg Leu Met Gln Ile Ile

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Ser Val Thr Ala Leu Val Thr Lys Ser Asp Thr Arg Ala Ala Asp Phe		
	485	490 495
Phe Val Val Pro Thr Gly Ser His Phe Tyr Leu Arg Val Lys Val Lys		
	500	505 510
Asp Ser Gly Ala Gly Ile Asn Pro Gln Asp Ile Pro Lys Ile Phe Thr		
	515	520 525
Lys Phe Ala Gln Thr Gln Ser Leu Ala Thr Arg Ser Ser Gly Gly Ser		
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Gly Leu Gly Leu Ala Ile Ser Lys Arg Phe Val Asn Leu Met Glu Gly		
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Asn Ile Trp Ile Glu Ser Asp Gly Leu Gly Lys Gly Cys Thr Ala Ile		
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Phe Asp Val Lys Leu Gly Ile Ser Glu Arg Ser Asn Glu Ser Lys Gln		
	580	585 590
Ser Gly Ile Pro Lys Val Pro Ala Ile Pro Arg His Ser Asn Phe Thr		
	595	600 605
Gly Leu Lys Val Leu Val Met Asp Glu Asn Gly Val Ser Arg Met Val		
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Thr Lys Gly Leu Leu Val His Leu Gly Cys Glu Val Thr Thr Val Ser		
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Ser Asn Glu Glu Cys Leu Arg Val Val Ser His Glu His Lys Val Val		
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Phe Met Asp Val Cys Met Pro Gly Val Glu Asn Tyr Gln Ile Ala Leu		
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Arg Ile His Glu Lys Phe Thr Lys Gln Arg His Gln Arg Pro Leu Leu		
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Ser Phe Gly Leu Asp Gly Val Leu Leu Lys Pro Val Ser Leu Asp Asn		
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Gly Met		

<210> 2
 <211> 738
 <212> PRT
 <213> pLBS107 construct

<400> 2

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Phe Ser Ile Pro Leu Glu Leu Ile Tyr Phe Val Lys Lys Ser Ala Val
          35           40           45

Phe Pro Tyr Arg Trp Val Leu Val Gln Phe Gly Ala Phe Ile Val Leu
          50           55           60

Tyr Gly Ala Thr His Leu Ile Asn Leu Trp Thr Phe Thr Thr His Ser
65           70           75           80

Arg Thr Val Ala Leu Val Met Thr Thr Ala Lys Val Leu Thr Ala Val
          85           90           95

Val Ser Cys Ala Thr Thr Leu Met Leu Val His Ile Ile Pro Asp Leu
          100          105          110

Leu Ser Val Lys Thr Arg Glu Leu Phe Leu Lys Asn Lys Ala Ala Glu
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Leu Asp Arg Glu Met Gly Leu Ile Arg Thr Gln Glu Glu Thr Gly Arg
          130          135          140

His Val Arg Met Leu Thr His Glu Ile Arg Ser Thr Leu Asp Arg His
145          150          155          160

Thr Ile Leu Lys Thr Thr Leu Val Glu Leu Gly Arg Thr Leu Ala Leu
          165          170          175

Glu Glu Cys Ala Leu Trp Met Pro Thr Arg Thr Gly Leu Glu Leu Gln
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Leu Ser Tyr Thr Leu Arg His Gln His Pro Val Glu Tyr Thr Val Pro
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Ile Gln Leu Pro Val Ile Asn Gln Val Phe Gly Thr Ser Arg Ala Val
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Lys Ile Ser Pro Asn Ser Pro Val Ala Arg Leu Arg Pro Val Ser Gly
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Lys Tyr Met Leu Gly Glu Val Val Ala Val Arg Val Pro Leu Leu His
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 Tyr Ala Leu Met Val Leu Met Leu Pro Ser Asp Ser Ala Arg Gln Trp
 275 280 285
 His Val His Glu Leu Glu Leu Val Glu Val Val Ala Asp Gln Val Ala
 290 295 300
 Val Ala Leu Ser His Ala Ala Ile Leu Glu Glu Ser Met Arg Ala Arg
 305 310 315 320
 Asp Leu Leu Met Glu Gln Asn Val Ala Leu Asp Leu Ala Arg Arg Glu
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 Ala Glu Thr Ala Ile Arg Ala Arg Asn Asp Phe Leu Ala Val Met Asn
 340 345 350
 His Glu Met Arg Thr Pro Met His Ala Ile Ile Ala Leu Ser Ser Leu
 355 360 365
 Leu Gln Glu Thr Glu Leu Thr Pro Glu Gln Arg Leu Met Val Glu Thr
 370 375 380
 Ile Leu Lys Ser Ser Asn Leu Leu Ala Thr Leu Met Asn Asp Val Leu
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 Phe Asn Leu His Thr Leu Phe Arg Glu Val Leu Asn Leu Ile Lys Pro
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 Lys Phe Ala Gln Thr Gln Ser Leu Ala Thr Arg Ser Ser Gly Gly Ser
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 Phe Asp Val Lys Leu Gly Ile Ser Glu Arg Ser Asn Glu Ser Lys Gln
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 Ser Gly Ile Pro Lys Val Pro Ala Ile Pro Arg His Ser Asn Phe Thr
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 Ser Asn Glu Glu Cys Leu Arg Val Val Ser His Glu His Lys Val Val
 645 650 655
 Phe Met Asp Val Cys Met Pro Gly Val Glu Asn Tyr Gln Ile Ala Leu
 660 665 670
 Arg Ile His Glu Lys Phe Thr Lys Gln Arg His Gln Arg Pro Leu Leu
 675 680 685
 Val Ala Leu Ser Gly Asn Thr Asp Lys Ser Thr Lys Glu Lys Cys Met
 690 695 700
 Ser Phe Gly Leu Asp Gly Val Leu Leu Lys Pro Val Ser Leu Asp Asn
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 Ile Arg Asp Val Leu Ser Asp Leu Leu Glu Pro Arg Val Leu Tyr Glu
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Gly Met

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 <212> PRT
 <213> pLBS107 construct

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 Phe Ser Ile Pro Leu Glu Leu Ile Tyr Phe Val Lys Lys Ser Ala Val
 35 40 45

Phe Pro Tyr Arg Trp Val Leu Val Gln Phe Gly Ala Phe Ile Val Leu
 50 55 60
 Tyr Gly Ala Thr His Leu Ile Asn Leu Trp Thr Phe Thr Thr His Ser
 65 70 75 80
 Arg Thr Val Ala Leu Val Met Thr Thr Ala Lys Val Leu Thr Ala Val
 85 90 95
 Val Ser Cys Ala Thr Ala Leu Met Leu Val His Ile Ile Pro Asp Leu
 100 105 110
 Leu Ser Val Lys Thr Arg Glu Leu Phe Leu Lys Asn Lys Ala Ala Glu
 115 120 125
 Leu Asp Arg Glu Met Gly Leu Ile Arg Thr Gln Glu Glu Thr Gly Arg
 130 135 140
 His Val Arg Met Leu Thr His Glu Ile Arg Ser Thr Leu Asp Arg His
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 Thr Ile Leu Lys Thr Thr Leu Val Glu Leu Gly Arg Thr Leu Ala Leu
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 Glu Glu Cys Ala Leu Trp Met Pro Thr Arg Thr Gly Leu Glu Leu Gln
 180 185 190
 Leu Ser Tyr Thr Leu Arg His Gln His Pro Val Glu Tyr Thr Val Pro
 195 200 205
 Ile Gln Leu Pro Val Ile Asn Gln Val Phe Gly Thr Ser Arg Ala Val
 210 215 220
 Lys Ile Ser Pro Asn Ser Pro Val Ala Arg Leu Arg Pro Val Ser Gly
 225 230 235 240
 Lys Tyr Met Leu Gly Glu Val Val Ala Val Arg Val Pro Leu Leu His
 245 250 255
 Leu Ser Asn Phe Gln Ile Asn Asp Trp Pro Glu Leu Ser Thr Lys Arg
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 Tyr Ala Leu Met Val Leu Met Leu Pro Ser Asp Ser Ala Arg Gln Trp
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 His Val His Glu Leu Glu Leu Val Glu Val Val Ala Asp Gln Val Ala
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 Val Ala Leu Ser His Ala Ala Ile Leu Glu Glu Ser Met Arg Ala Arg
 305 310 315 320
 Asp Leu Leu Met Glu Gln Asn Val Ala Leu Asp Leu Ala Arg Arg Glu
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 Ala Glu Thr Ala Ile Arg Ala Arg Asn Asp Phe Leu Ala Val Met Asn

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Ile Leu Lys Ser Ser Asn Leu Leu	Ala Thr Leu Met Asn Asp Val	Leu
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Asp Leu Ser Arg Leu Glu Asp Gly	Ser Leu Gln Leu Glu Leu Gly	Thr
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450	455	460
Leu Asn Ile Val Gly Asn Ala Val	Lys Phe Ser Lys Gln Gly Ser	Ile
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Ser Val Thr Ala Leu Val Thr Lys	Ser Asp Thr Arg Ala Ala Asp	Phe
485	490	495
Phe Val Val Pro Thr Gly Ser His	Phe Tyr Leu Arg Val Lys Val	Lys
500	505	510
Asp Ser Gly Ala Gly Ile Asn Pro	Gln Asp Ile Pro Lys Ile Phe	Thr
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Lys Phe Ala Gln Thr Gln Ser Leu	Ala Thr Arg Ser Ser Gly Gly	Ser
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Gly Leu Gly Leu Ala Ile Ser Lys	Arg Phe Val Asn Leu Met Glu	Gly
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Asn Ile Trp Ile Glu Ser Asp Gly	Leu Gly Lys Gly Cys Thr Ala	Ile
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Phe Asp Val Lys Leu Gly Ile Ser	Glu Arg Ser Asn Glu Ser Lys	Gln
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Ser Gly Ile Pro Lys Val Pro Ala	Ile Pro Arg His Ser Asn Phe	Thr
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Gly Leu Lys Val Leu Val Met Asp	Glu Asn Gly Val Ser Arg Met	Val
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Thr Lys Gly Leu Leu Val His Leu	Gly Cys Glu Val Thr Thr Val	Ser
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Ser Asn Glu Glu Cys Leu Arg Val Val Ser His Glu His Lys Val Val
 645 650 655
 Phe Met Asp Val Cys Met Pro Gly Val Glu Asn Tyr Gln Ile Ala Leu
 660 665 670
 Arg Ile His Glu Lys Phe Thr Lys Gln Arg His Gln Arg Pro Leu Leu
 675 680 685
 Val Ala Leu Ser Gly Asn Thr Asp Lys Ser Thr Lys Glu Lys Cys Met
 690 695 700
 Ser Phe Gly Leu Asp Gly Val Leu Leu Lys Pro Val Ser Leu Asp Asn
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Gly Met

<210> 4
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 35 40 45
 Phe Pro Tyr Arg Trp Val Leu Val Gln Phe Gly Ala Phe Phe Val Leu
 50 55 60
 Tyr Gly Ala Thr His Leu Ile Asn Leu Trp Thr Phe Thr Thr His Ser
 65 70 75 80
 Arg Thr Val Ala Leu Val Met Thr Thr Ala Lys Val Leu Thr Ala Val
 85 90 95
 Val Ser Cys Ala Thr Ala Leu Met Leu Val His Ile Ile Pro Asp Leu
 100 105 110
 Leu Ser Val Lys Thr Arg Glu Leu Phe Leu Lys Asn Lys Ala Ala Glu
 115 120 125
 Leu Asp Arg Glu Met Gly Leu Ile Arg Thr Gln Glu Glu Thr Gly Arg
 130 135 140

His Val Arg Met Leu Thr His Glu Ile Arg Ser Thr Leu Asp Arg His
 145 150 155 160
 Thr Ile Leu Lys Thr Thr Leu Val Glu Leu Gly Arg Thr Leu Ala Leu
 165 170 175
 Glu Glu Cys Ala Leu Trp Met Pro Thr Arg Thr Gly Leu Glu Leu Gln
 180 185 190
 Leu Ser Tyr Thr Leu Arg His Gln His Pro Val Glu Tyr Thr Val Pro
 195 200 205
 Ile Gln Leu Pro Val Ile Asn Gln Val Phe Gly Thr Ser Arg Ala Val
 210 215 220
 Lys Ile Ser Pro Asn Ser Pro Val Ala Arg Leu Arg Pro Val Ser Gly
 225 230 235 240
 Lys Tyr Met Leu Gly Glu Val Val Ala Val Arg Val Pro Leu Leu His
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 Leu Ser Asn Phe Gln Ile Asn Asp Trp Pro Glu Leu Ser Thr Lys Arg
 260 265 270
 Tyr Ala Leu Met Val Leu Met Leu Pro Ser Asp Ser Ala Arg Gln Trp
 275 280 285
 His Val His Glu Leu Glu Leu Val Glu Val Val Ala Asp Gln Val Ala
 290 295 300
 Val Ala Leu Ser His Ala Ala Ile Leu Glu Glu Ser Met Arg Ala Arg
 305 310 315 320
 Asp Leu Leu Met Glu Gln Asn Val Ala Leu Asp Leu Ala Arg Arg Glu
 325 330 335
 Ala Glu Thr Ala Ile Arg Ala Arg Asn Asp Phe Leu Ala Val Met Asn
 340 345 350
 His Glu Met Arg Thr Pro Met His Ala Ile Ile Ala Leu Ser Ser Leu
 355 360 365
 Leu Gln Glu Thr Glu Leu Thr Pro Glu Gln Arg Leu Met Val Glu Thr
 370 375 380
 Ile Leu Lys Ser Ser Asn Leu Leu Ala Thr Leu Met Asn Asp Val Leu
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 Asp Leu Ser Arg Leu Glu Asp Gly Ser Leu Gln Leu Glu Leu Gly Thr
 405 410 415
 Phe Asn Leu His Thr Leu Phe Arg Glu Val Leu Asn Leu Ile Lys Pro
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Ile Ala Val Val Lys Lys Leu Pro Ile Thr Leu Asn Leu Ala Pro Asp
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 Leu Asn Ile Val Gly Asn Ala Val Lys Phe Ser Lys Gln Gly Ser Ile
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 Ser Val Thr Ala Leu Val Thr Lys Ser Asp Thr Arg Ala Ala Asp Phe
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 Lys Phe Ala Gln Thr Gln Ser Leu Ala Thr Arg Ser Ser Gly Gly Ser
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 565 570 575
 Phe Asp Val Lys Leu Gly Ile Ser Glu Arg Ser Asn Glu Ser Lys Gln
 580 585 590
 Ser Gly Ile Pro Lys Val Pro Ala Ile Pro Arg His Ser Asn Phe Thr
 595 600 605
 Gly Leu Lys Val Leu Val Met Asp Glu Asn Gly Val Ser Arg Met Val
 610 615 620
 Thr Lys Gly Leu Leu Val His Leu Gly Cys Glu Val Thr Thr Val Ser
 625 630 635 640
 Ser Asn Glu Glu Cys Leu Arg Val Val Ser His Glu His Lys Val Val
 645 650 655
 Phe Met Asp Val Cys Met Pro Gly Val Glu Asn Tyr Gln Ile Ala Leu
 660 665 670
 Arg Ile His Glu Lys Phe Thr Lys Gln Arg His Gln Arg Pro Leu Leu
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 Val Ala Leu Ser Gly Asn Thr Asp Lys Ser Thr Lys Glu Lys Cys Met
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 Ser Phe Gly Leu Asp Gly Val Leu Leu Lys Pro Val Ser Leu Asp Asn
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 Ile Arg Asp Val Leu Ser Asp Leu Leu Glu Pro Arg Val Leu Tyr Glu

725

730

735

Gly Met

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 Phe Ser Ile Pro Leu Glu Leu Ile Tyr Phe Val Lys Lys Ser Ala Val
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 Phe Pro Tyr Arg Trp Val Leu Val Gln Phe Gly Ala Phe Ile Val Leu
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 Tyr Gly Ala Thr His Leu Ile Asn Leu Trp Thr Phe Thr Thr His Ser
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 Arg Thr Val Ala Leu Val Met Thr Thr Ala Lys Val Leu Thr Ala Val
 85 90 95
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 Val Ser Cys Ala Thr Ala Leu Met Leu Val His Ile Ile Pro Asp Leu
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 Leu Ser Val Lys Thr Arg Glu Leu Phe Leu Lys Asn Lys Ala Ala Glu
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 ctc gat aga gaa atg gga ttg att cga act cag gaa gaa acc gga agg 432
 Leu Asp Arg Glu Met Gly Leu Ile Arg Thr Gln Glu Glu Thr Gly Arg
 130 135 140
 cat gtg aga atg ttg act cat gag att aga agc act tta gat aga cat 480
 His Val Arg Met Leu Thr His Glu Ile Arg Ser Thr Leu Asp Arg His
 145 150 155 160

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Leu Ser Tyr Thr Leu Arg His Gln His Pro Val Glu Tyr Thr Val Pro	
195 200 205	
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Ile Gln Leu Pro Val Ile Asn Gln Val Phe Gly Thr Ser Arg Ala Val	
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Lys Ile Ser Pro Asn Ser Pro Val Ala Arg Leu Arg Pro Val Ser Gly	
225 230 235 240	
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Tyr Ala Leu Met Val Leu Met Leu Pro Ser Asp Ser Ala Arg Gln Trp	
275 280 285	
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His Val His Glu Leu Glu Leu Val Glu Val Val Ala Asp Gln Val Ala	
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Val Ala Leu Ser His Ala Ala Ile Leu Glu Glu Ser Met Arg Ala Arg	
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Asp Leu Leu Met Glu Gln Asn Val Ala Leu Asp Leu Ala Arg Arg Glu	
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ttt gat gtt aaa ctt ggg atc tca gaa cgt tca aac gaa tct aaa cag Phe Asp Val Lys Leu Gly Ile Ser Glu Arg Ser Asn Glu Ser Lys Gln 580 585 590	1776
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<210> 6
<211> 773
<212> PRT
<213> Amino acid sequence alignment of ETR2

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			20					25					30		
Asn	Cys	Glu	Asp	Glu	Gly	Asn	Ser	Phe	Trp	Ser	Thr	Glu	Asn	Ile	Leu
		35					40					45			
Glu	Thr	Gln	Arg	Val	Ser	Asp	Phe	Leu	Ile	Ala	Val	Ala	Tyr	Phe	Ser
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Ile Pro Ile Glu Leu Leu Tyr Phe Val Ser Cys Ser Asn Val Pro Phe
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Lys Trp Val Leu Phe Glu Phe Ile Ala Phe Ile Val Leu Cys Gly Met
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Thr His Leu Leu His Gly Trp Thr Tyr Ser Ala His Pro Phe Arg Leu
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Met Met Ala Phe Thr Val Phe Lys Met Leu Thr Ala Leu Val Ser Cys
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Ala Thr Ala Ile Thr Leu Ile Thr Leu Ile Pro Leu Leu Leu Lys Val
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Lys Val Arg Glu Phe Met Leu Lys Lys Lys Ala His Glu Leu Gly Arg
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Glu Val Gly Leu Ile Leu Ile Lys Lys Glu Thr Gly Phe His Val Arg
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Met Leu Thr Gln Glu Ile Arg Lys Ser Leu Asp Arg His Thr Ile Leu
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Tyr Thr Thr Leu Val Glu Leu Ser Lys Thr Leu Gly Leu Gln Asn Cys
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Ala Val Trp Met Pro Asn Asp Gly Gly Thr Glu Met Asp Leu Thr His
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Asp Leu Asp Val Val Arg Ile Arg Glu Ser Asp Glu Val Asn Val Leu
245              250              255

Ser Val Asp Ser Ser Ile Ala Arg Ala Ser Gly Gly Gly Gly Asp Val
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275              280              285

Ser Asp Phe Asn Gly Glu Leu Ser Tyr Ala Ile Leu Val Cys Val Leu
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Pro Gly Gly Thr Pro Arg Asp Trp Thr Tyr Gln Glu Ile Glu Ile Val
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Leu Glu Glu Ser Gln Leu Met Arg Glu Lys Leu Ala Glu Gln Asn Arg
340              345              350

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 Asn Ala Phe Gln Lys Thr Met Ser Glu Gly Met Arg Arg Pro Met His
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 385 390 395 400
 Glu Gln Lys Met Ile Val Asp Thr Met Val Lys Thr Gly Asn Val Met
 405 410 415
 Ser Asn Leu Val Gly Asp Ser Met Asp Val Pro Asp Gly Arg Phe Gly
 420 425 430
 Thr Glu Met Lys Pro Phe Ser Leu His Arg Thr Ile His Glu Ala Ala
 435 440 445
 Cys Met Ala Arg Cys Leu Cys Leu Cys Asn Gly Ile Arg Phe Leu Val
 450 455 460
 Asp Ala Glu Lys Ser Leu Pro Asp Asn Val Val Gly Asp Glu Arg Arg
 465 470 475 480
 Val Phe Gln Val Ile Leu His Ile Val Gly Ser Leu Val Lys Pro Arg
 485 490 495
 Lys Arg Gln Glu Gly Ser Ser Leu Met Phe Lys Val Leu Lys Glu Arg
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 Gly Ser Leu Asp Arg Ser Asp His Arg Trp Ala Ala Trp Arg Ser Pro
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 Ala Ser Ser Ala Asp Gly Asp Val Tyr Ile Arg Phe Glu Met Asn Val
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 Asp Gln Glu Val Gly Asp Val Arg Phe Ser Gly Gly Tyr Gly Leu Gly
 565 570 575
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 Ser Leu Leu Leu Arg Phe Arg Arg Arg Pro Ser Ile Ser Val His Gly
 610 615 620
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 Ser Leu Leu Arg Gly Leu Gln Val Leu Leu Val Asp Thr Asn Asp Ser

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Thr	Ala	Val	Ser	Ser	Gly	Phe	Asp	Cys	Leu	Thr	Ala	Ile	Ala	Pro	Gly
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Met	Ala	Glu	Met	Asp	Gly	Tyr	Glu	Val	Ala	Met	Arg	Ile	Arg	Ser	Arg
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Ser	Trp	Pro	Leu	Ile	Val	Ala	Thr	Thr	Val	Ser	Leu	Asp	Glu	Glu	Met
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Trp	Asp	Lys	Cys	Ala	Gln	Ile	Gly	Ile	Asn	Gly	Val	Val	Arg	Lys	Pro
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<210> 7
 <211> 2893
 <212> DNA
 <213> Amino acid sequence alignment of ETR2

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 gaaactcaaa gagtaagcga tttcttaatc gcagtagctt atttctcaat ccctattgag 600
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<210> 8
<211> 1622
<212> DNA
<213> pLBS107 construct

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<210> 9
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<212> DNA
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aattcaatcc tttgaattgt taaatatata atatatgttt aatgtcttcc tgttttaacc 360
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tcgatatctt atgtaggtaa ctatgtttcg taatacatag aattgttcaa ctttttttat	600
gttcgaactt ttttttaatt tgcaatgtaa ttatttgtct tatgttacat tttagtcatt	660
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Ser Ile Pro Leu Glu Leu Ile Tyr Phe Val Lys Lys Ser Ala Val Phe	
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Gly Ala Thr His Leu Ile Asn Leu Trp Thr Phe Thr Thr His Ser Arg	
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Ile Ser Pro Asn Ser Pro Val Ala Arg Leu Arg Pro Val Ser Gly Lys	
230 235 240	
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Tyr Met Leu Gly Glu Val Val Ala Val Arg Val Pro Leu Leu His Leu	
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Val His Glu Leu Glu Leu Val Glu Val Val Ala Asp Gln Val Ala Val			
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Ala Leu Ser His Ala Ala Ile Leu Glu Glu Ser Met Arg Ala Arg Asp			
310	315	320	
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Leu Leu Met Glu Gln Asn Val Ala Leu Asp Leu Ala Arg Arg Glu Ala			
325	330	335	
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Glu Thr Ala Ile Arg Ala Arg Asn Asp Phe Leu Ala Val Met Asn His			
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Glu Met Arg Thr Pro Met His Ala Ile Ile Ala Leu Ser Ser Leu Leu			
355	360	365	
caa gaa acg gaa cta acc cct gaa caa aga ctg atg gtg gaa aca ata			2828
Gln Glu Thr Glu Leu Thr Pro Glu Gln Arg Leu Met Val Glu Thr Ile			
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Leu Lys Ser Ser Asn Leu Leu Ala Thr Leu Met Asn Asp Val Leu Asp			
390	395	400	
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Pro Glu Phe Val Val Gly Asp Glu Lys Arg Leu Met Gln Ile Ile Leu			
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Phe Ala Gln Thr Gln Ser Leu Ala Thr Arg Ser Ser Gly Gly Ser Gly	
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Leu Gly Leu Ala Ile Ser Lys Arg Phe Val Asn Leu Met Glu Gly Asn	
550 555 560	
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Asp Val Lys Leu Gly Ile Ser Glu Arg Ser Asn Glu Ser Lys Gln Ser	
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Gly Ile Pro Lys Val Pro Ala Ile Pro Arg His Ser Asn Phe Thr Gly	
595 600 605	
ctt aag gtt ctt gtc atg gat gag aac ggg gta agt aga atg gtg acg	3548
Leu Lys Val Leu Val Met Asp Glu Asn Gly Val Ser Arg Met Val Thr	
610 615 620 625	
aag gga ctt ctt gta cac ctt ggg tgc gaa gtg acc acg gtg agt tca	3596
Lys Gly Leu Leu Val His Leu Gly Cys Glu Val Thr Thr Val Ser Ser	
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Asn Glu Glu Cys Leu Arg Val Val Ser His Glu His Lys Val Val Phe	
645 650 655	
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Met Asp Val Cys Met Pro Gly Val Glu Asn Tyr Gln Ile Ala Leu Arg	
660 665 670	
att cac gag aaa ttc aca aaa caa cgc cac caa cgg cca cta ctt gtg	3740
Ile His Glu Lys Phe Thr Lys Gln Arg His Gln Arg Pro Leu Leu Val	
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Ala Leu Ser Gly Asn Thr Asp Lys Ser Thr Lys Glu Lys Cys Met Ser	
690 695 700 705	

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Phe Gly Leu Asp Gly Val Leu Leu Lys Pro Val Ser Leu Asp Asn Ile	
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Arg Asp Val Leu Ser Asp Leu Leu Glu Pro Arg Val Leu Tyr Glu Gly	
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